In the Specification:

Please replace the paragraph beginning at page 5, line 26, with the following:

--Figure 1: Figure 1A shows an amino acid of human wild-type TRAC1 (SEQ ID NO:1); Figure 1B shows a cDNA sequence of human wild-type TRAC1 (SEQ ID NO:2); Figure 1C shows a second, slightly shorter cDNA sequence of human wild type TRAC1 (SEQ ID NO:3); Figure 1D shows a cDNA sequence encoding a truncated version of TRAC1 (SEQ ID NO:4; nucleotides 127-891 of SEQ ID NO:3); Figure 1E shows a genomic sequence of human wild type TRAC1 (SEQ ID NO:5); and Figure 1F shows a cDNA (SEQ ID NO:6) and amino acid sequence (SEQ ID NO:7) for mouse wild type TRAC1.--

Please replace the paragraph beginning at page 6, line 11, with the following:

--Figure 7 shows that TRAC1 (FLJ20456) (SEQ ID NO:1) is similar to two sequences (SEQ ID NOS:8 and 9) with ring domains.--

Please replace the paragraph beginning at page 6, line 21, with the following:

--Figure 13A shows point mutations in conserved cysteine residues of the TRAC1 ring finger domain (SEQ ID NOS:10-17). Figure 13B shows point mutations in the conserved cysteine residues of the TRAC1 ring finger domain disrupt ligase activity.--

Please replace the paragraph beginning at page 12, line 30, with the following:

--The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences

that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (i.e., about 60% identity, preferably 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region (e.g., a nucleotide sequence of SEQ ID NO:2), when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (*see, e.g.*, NCBI web site http://www.ncbi.nlm.nih.gov/BLAST/ or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the compliment of a test sequence. The definition also includes sequences that have deletions and/or additions, as well as those that have substitutions. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.--

Please replace the paragraph beginning at page 39, line 22, with the following:

--Common linkers such as peptides, polyethers, and the like can also serve as tags, and include polypeptide sequences, such as poly Gly sequences of between about 5 and 200 amino acids (SEQ ID NO:18). Such flexible linkers are known to persons of skill in the art. For example, poly(ethelyne glycol) linkers are available from Shearwater Polymers, Inc. Huntsville, Alabama. These linkers optionally have amide linkages, sulfhydryl linkages, or heterofunctional linkages.--

Please insert the accompanying paper copy of the Sequence Listing, page numbers 1 to 13, at the end of the application.